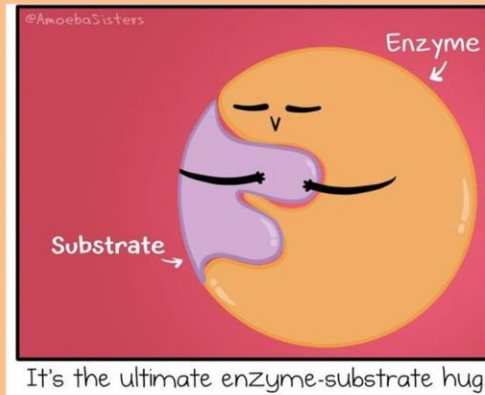
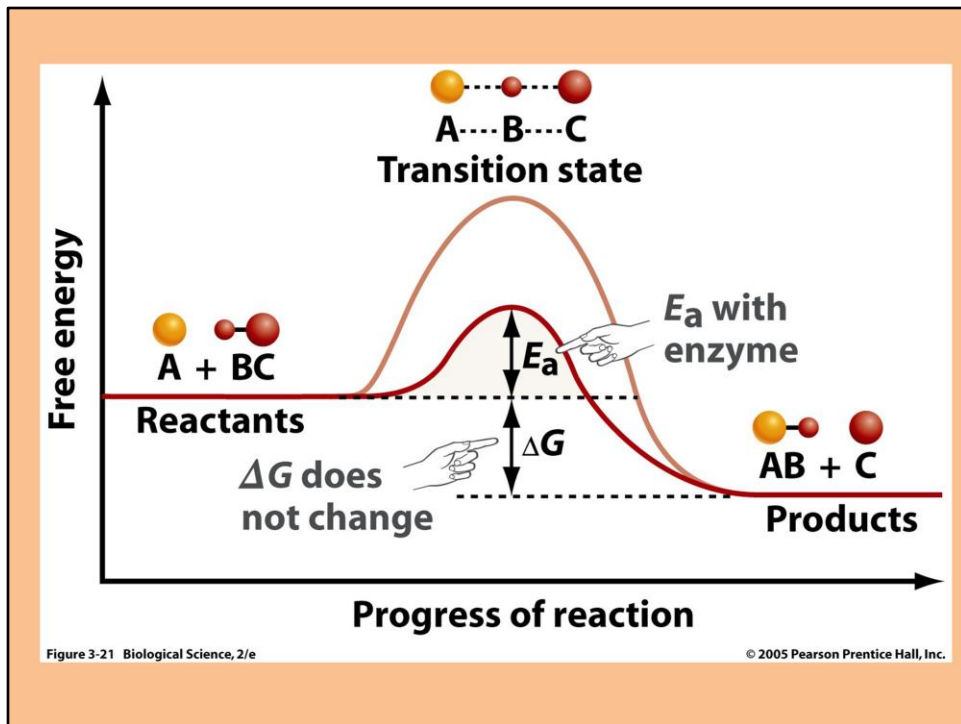


# Enzymes





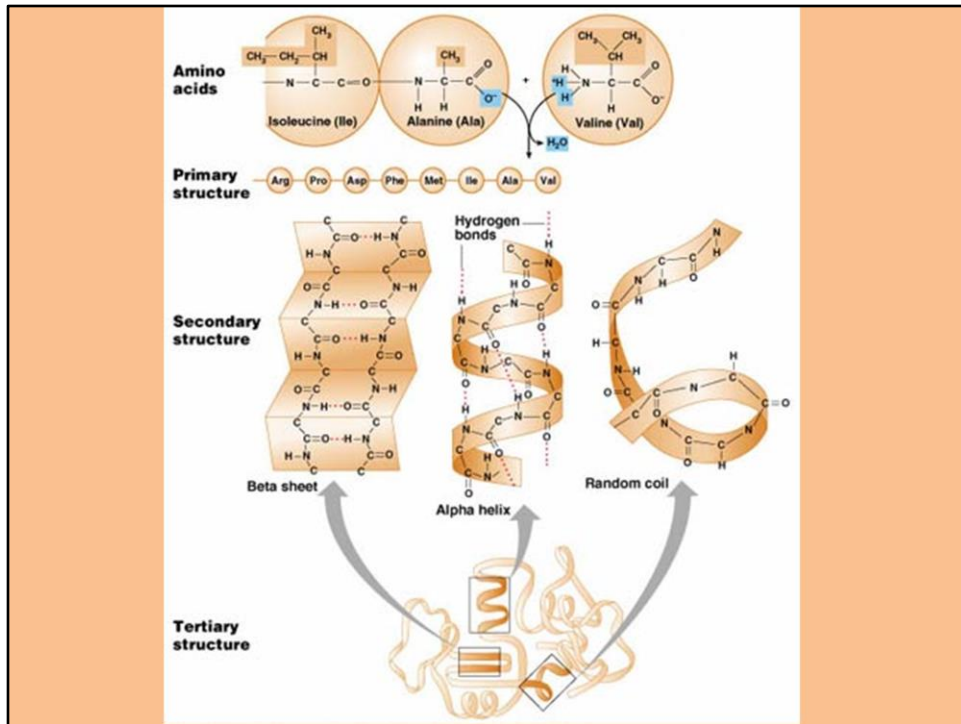
Enzymes DO change \_\_\_\_\_

\_\_\_\_\_

Enzymes DO NOT change \_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_



Primary structure: \_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_

Secondary structure: \_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_

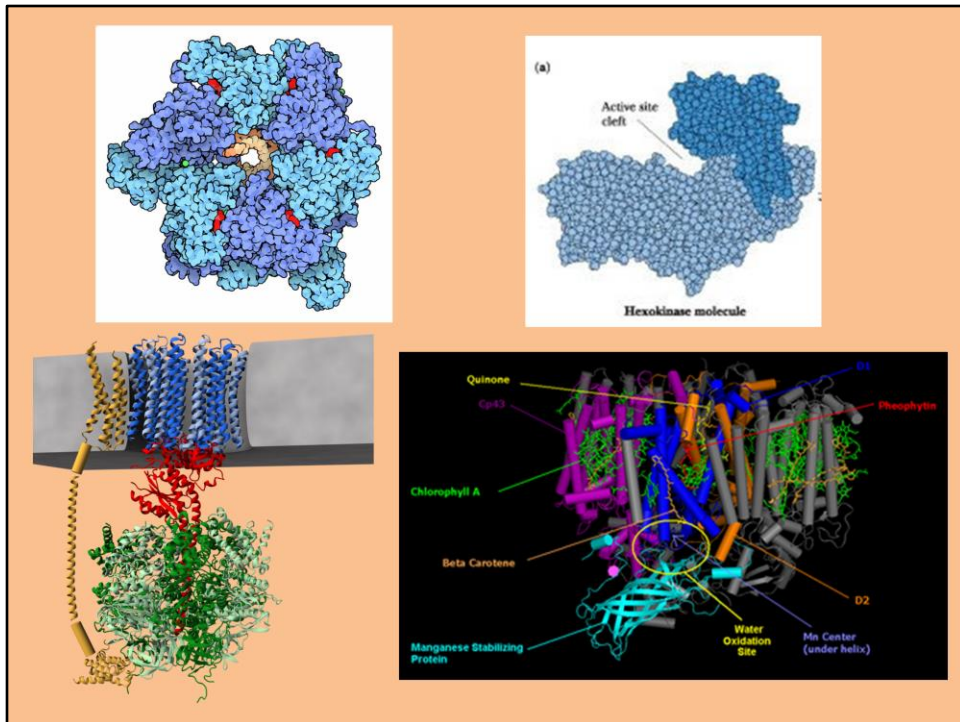
\_\_\_\_\_

Tertiary structure: \_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_



Overall structure of protein enzymes depend on bonds being held at specific places. This is determined by an enzymes:

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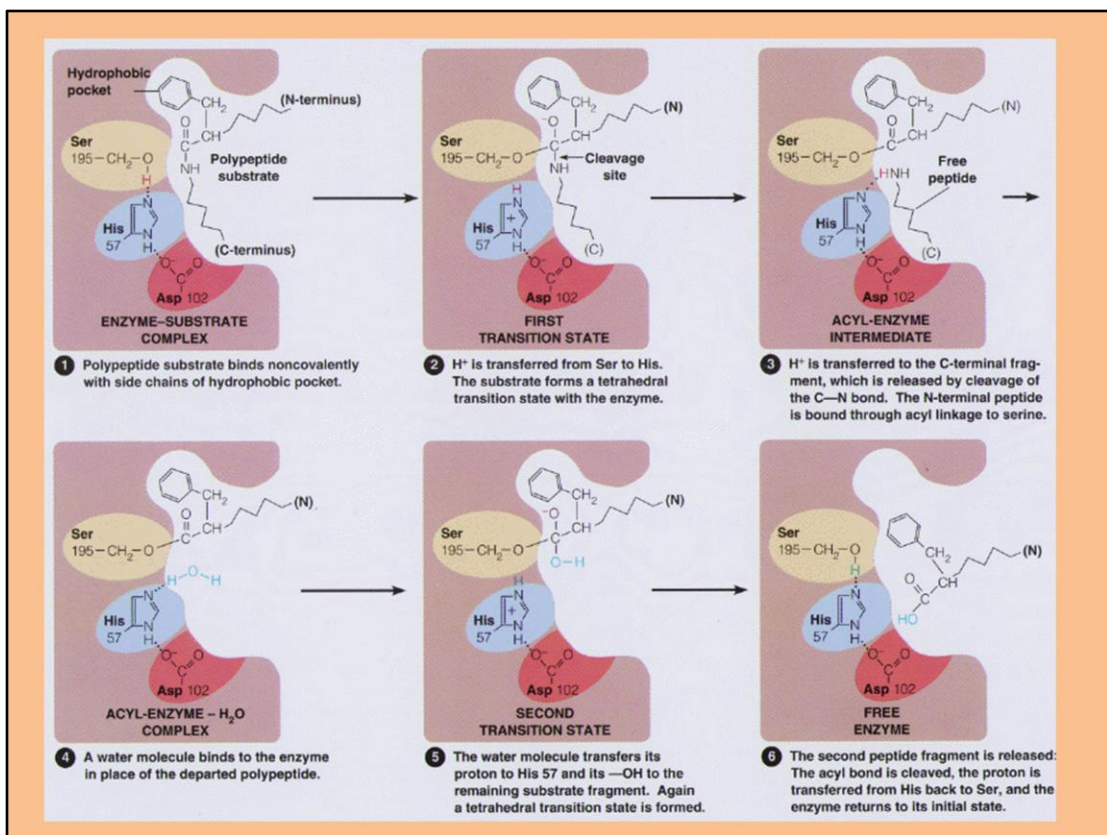
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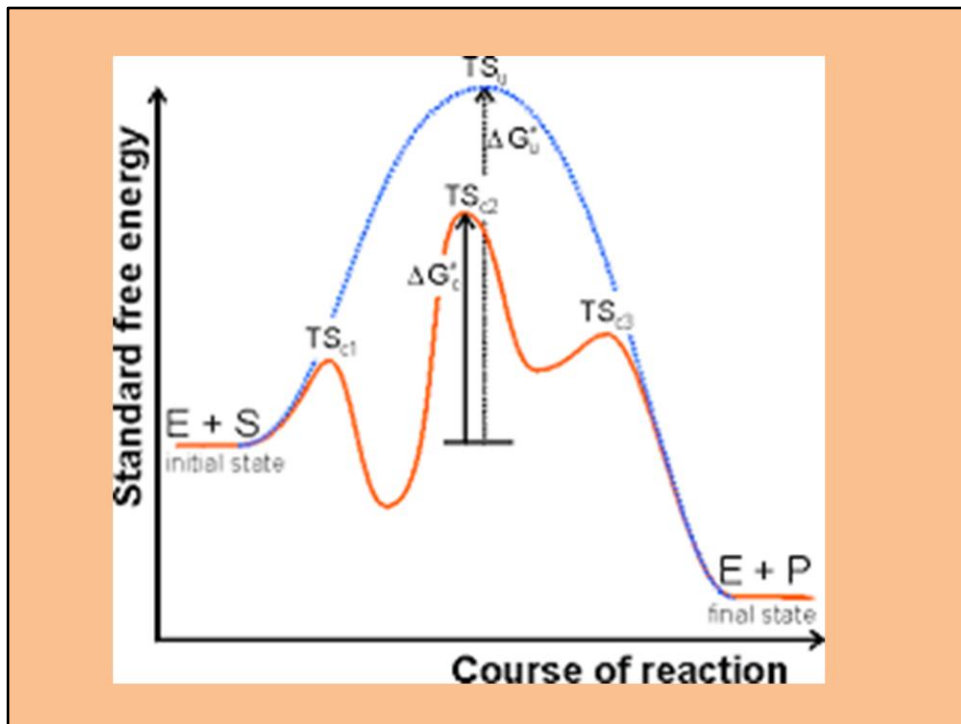


## The Active Site & Mechanisms of Enzyme Action

1. Favorable initial binding interactions draw substrates in.
2. Unstable bonds formed, make likely to react (change).

The active site's catalytic properties are determined by its amino acids & their interactions with other nearby molecules.

Some enzymes are very specific, others very generic.



Reaction without enzyme takes longer because:

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Enzymes lower  $E_a$  by: \_\_\_\_\_

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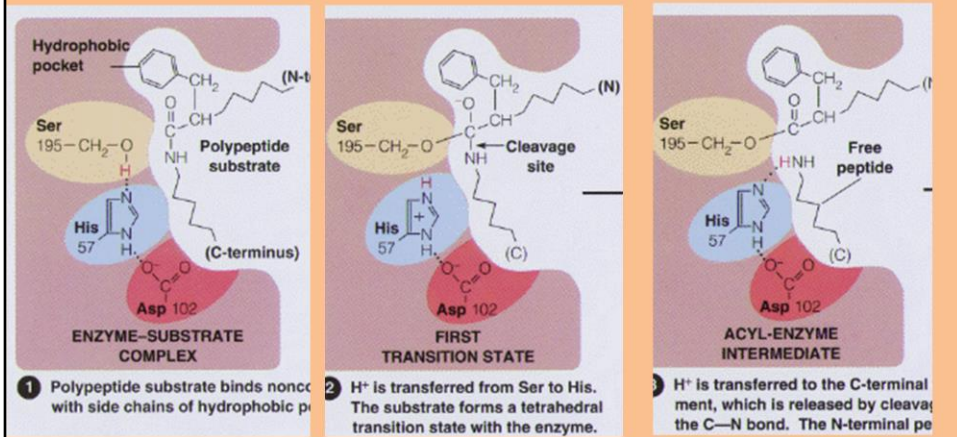
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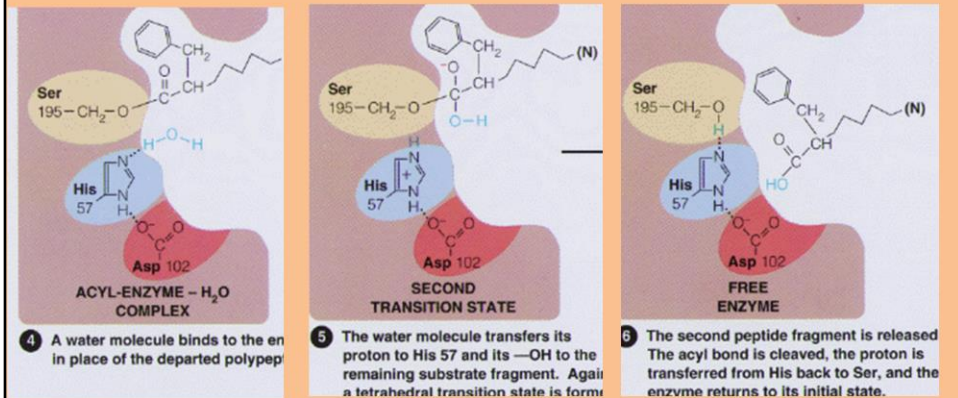
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- **High Temperature:** deform hydrogen bond between Ser & His, enzyme denatures (Step 1).
- **Bases:** Selectively remove & add  $H^+$  to themselves. Cause  $H^+$  to transfer from Ser to itself rather than to His. Interferes with reaction rate (Step 2).

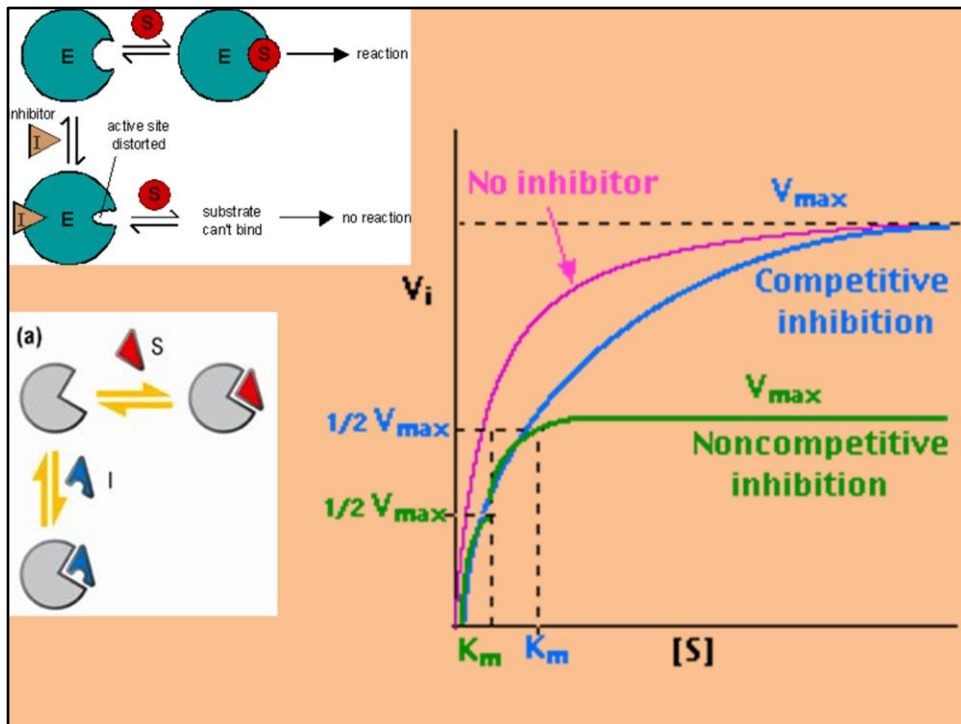




- **Salts**: Bond strongly to other charged atoms. In His + state (step 5) a salt could bind irreversibly, making enzyme nonfunctional.
- **Acids**: Release H+. Instead of His & Asp re-hydrogen bonding, released H+ from an acid could bond with O- on Asp, changing the active site shape & reactivity.







Competitive Inhibition: \_\_\_\_\_

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Non- Competitive Inhibition: \_\_\_\_\_

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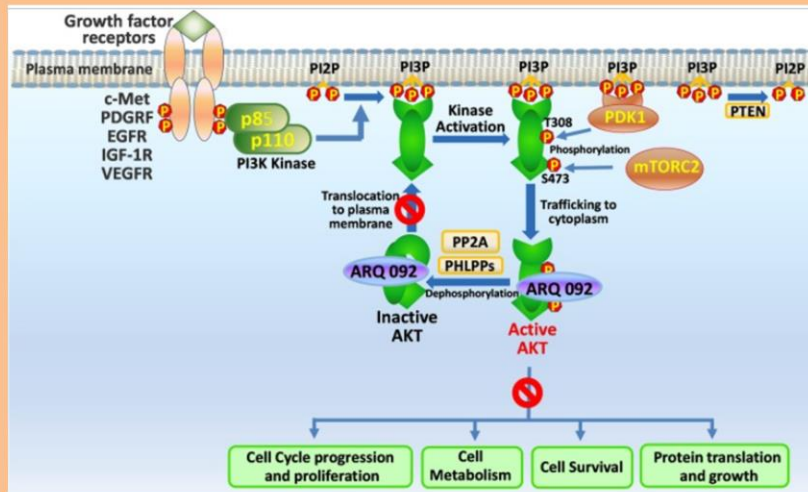
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Allosteric inhibition to treat cancer cells: **Miransertib** experimental cancer medication allosterically inhibits specific active kinases without causing many other downstream effects (stimulating other processes also leading to cancer as with some other drugs).



# Allosteric regulation in metabolism

